

FIG. 1A

GAATTCTCTGGACTGAGGCTCCAGTTCTGGCCTTTGGGG

TTCAAGATCACTGGGACCAGGCCGTGATCTCTATGCCCCGAGTCTCAACCCTCAACTGTC
ACCCCAAGGCACTTGGGACGTCTGGACAGACCGAGTCCCGGGAAGCCCCAGCACTGCC

GCTGCCACACTGCCCTGAGCCCAAATGGGGGAGTGAGAGGCCA TAG CTG TCT GGC

| | | | | | | |
|---|--|-----|--|-----|--|-----|
| S1 | | S5 | | S10 | | S15 |
| Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu | | | | | | |
| ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCA CTG GTG CTC | | | | | | |
| 216 | | 225 | | 234 | | 243 |

| | | | | | | | |
|---|--|-----|--|-----|--|-----|-----|
| | | S20 | | S25 | | S29 | 1 |
| Leu Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu | | | | | | | |
| CTG GAG CTG TTG GTG GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG | | | | | | | |
| 261 | | 270 | | 279 | | 288 | 297 |

| | | | | | | |
|---|--|-----|--|-----|--|-----|
| | | 5 | | 10 | | 15 |
| Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro | | | | | | |
| GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA GAT AGT GTG TGT CCC | | | | | | |
| 306 | | 315 | | 324 | | 333 |

| | | | | | | |
|---|--|-----|--|-----|--|-----|
| | | 20 | | 25 | | 30 |
| Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr | | | | | | |
| CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC | | | | | | |
| 351 | | 360 | | 369 | | 378 |

| | | | | | | |
|---|--|-----|--|-----|--|-----|
| | | 35 | | 40 | | 45 |
| Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro | | | | | | |
| AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG | | | | | | |
| 396 | | 405 | | 414 | | 423 |

| | | | | | | |
|---|--|-----|--|-----|--|-----|
| | | 50 | | 55 | | 60 |
| Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr | | | | | | |
| GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC | | | | | | |
| 441 | | 450 | | 459 | | 468 |

| | | | | | | |
|---|--|-----|--|-----|--|-----|
| | | 65 | | 70 | | 75 |
| Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys | | | | | | |
| GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA TGC | | | | | | |
| 486 | | 495 | | 504 | | 513 |

| | | | | | | |
|---|--|-----|--|-----|--|-----|
| | | 80 | | 85 | | 90 |
| Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp | | | | | | |
| CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC | | | | | | |
| 531 | | 540 | | 549 | | 558 |

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FIG. 1B

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|-----|-----|------|-----|-----|
| Arg | Asp | Thr | Val | Cys | Gly | Cys | Arg | Lys | Asn | Gln | Tyr | Arg | His | Tyr |
| CGG | GAC | ACC | GTG | TGT | GGC | TGC | AGG | AAG | AAC | CAG | TAC | CGG | CAT | TAT |
| 576 | | | 585 | | | 594 | | | 603 | | | 612 | | |
| Trp | Ser | Glu | Asn | Leu | Phe | Gln | Cys | Phe | Asn | Cys | Ser | Leu | Cys | Leu |
| TGG | AGT | GAA | AAC | CTT | TTC | CAG | TGC | TTC | AAT | TGC | AGC | CTC | TGC | CTC |
| 621 | | | 630 | | | 639 | | | 648 | | | 657 | | |
| Asn | Gly | Thr | Val | His | Leu | Ser | Cys | Gln | Glu | Lys | Gln | Asn | Thr | Val |
| AAT | GGG | ACC | GTG | CAC | CTC | TCC | TGC | CAG | GAG | AAA | CAG | AAC | ACC | GTG |
| 666 | | | 675 | | | 684 | | | 693 | | | 702 | | |
| Cys | Thr | Cys | His | Ala | Gly | Phe | Phe | Leu | Arg | Glu | Asn | Glu | Cys | Val |
| TGC | ACC | TGC | CAT | GCA | GGT | TTC | TTT | CTA | AGA | GAA | AAC | GAG | TGT | GTC |
| 711 | | | 720 | | | 729 | | | 738 | | | 747 | | |
| Ser | Cys | Ser | Asn | Cys | Lys | Lys | Ser | Leu | Glu | Cys | Thr | Lys | Leu | Cys |
| TCC | TGT | AGT | AAC | TGT | AAG | AAA | AGC | CTG | GAG | TGC | ACG | AAG | TTG | TGC |
| 756 | | | 765 | | | 774 | | | 783 | | | 792 | | |
| Leu | Pro | Gln | Ile | Glu | Asn | Val | Lys | Gly | Thr | Glu | Asp | Ser | Gly | Thr |
| CTA | CCC | CAG | ATT | GAG | AAT | GTT | AAG | GGC | ACT | GAG | GAC | TCA | GGC | ACC |
| 801 | | | 810 | | | 819 | | | 828 | | | 837 | | |
| Thr | Val | Leu | Leu | Pro | Leu | Val | Ile | Phe | Phe | Gly | Leu | Cys | Leu | Leu |
| ACA | GTG | CTG | TTG | CCC | CTG | GTC | ATT | TTC | TTT | GGT | CTT | TGC | CTT | TTA |
| 846 | | | 855 | | | 864 | | | 873 | | | 882 | | |
| Ser | Leu | Leu | Phe | Ile | Gly | Leu | Met | Tyr | Arg | Tyr | Gln | Arg | Trp | Lys |
| TCC | CTC | CTC | TTC | ATT | GGT | TTA | ATG | TAT | CGC | TAC | CAA | CGG | TGG | AAG |
| 891 | | | 900 | | | 909 | | | 918 | | | 927 | | |
| Ser | Lys | Leu | Tyr | Ser | Ile | Val | Cys | Gly | Lys | Ser | Thr | Pro | Glu | Lys |
| TCC | AAG | CTC | TAC | TCC | ATT | GTT | TGT | GGG | AAA | TCG | ACA | CCT | GAA | AAA |
| 936 | | | 945 | | | 954 | | | 963 | | | 972 | | |
| Glu | Gly | Glu | Leu | Glu | Gly | Thr | Thr | Thr | Lys | Pro | Leu | Ala | Pro | Asn |
| GAG | GGG | GAG | CTT | GAA | GGA | ACT | ACT | ACT | AAG | CCC | CTG | GCC | CCA | AAC |
| 981 | | | 990 | | | 999 | | | 1008 | | | 1017 | | |

FIG. 1C

| | | | | | | | | | | | | | | | | | |
|------|-----|-----|------|-----|-----|------|-----|-----|------|-----|-----|----------------|-----|-----|-----|-----|-----|
| Pro | Ser | Phe | 245 | Ser | Pro | Thr | Pro | Gly | 250 | Phe | Thr | Pro | Thr | Leu | Gly | 255 | Phe |
| CCA | AGC | TTC | AGT | CCC | ACT | CCA | GGC | TTC | ACC | CCC | ACC | CTG | GGC | TTC | | | |
| 1026 | | | 1035 | | | 1044 | | | 1053 | | | 1062 | | | | | |
| Ser | Pro | Val | 260 | Pro | Ser | Ser | Thr | Phe | 265 | Thr | Ser | Ser | Ser | Thr | Tyr | 270 | Thr |
| AGT | CCC | GTG | CCC | AGT | TCC | ACC | TTC | ACC | TCC | AGC | TCC | ACC | TAT | ACC | | | |
| 1071 | | | 1080 | | | 1089 | | | 1098 | | | 1107 | | | | | |
| Pro | Gly | Asp | 275 | Cys | Pro | Asn | Phe | Ala | 280 | Ala | Pro | Arg | Arg | Glu | Val | 285 | Ala |
| CCC | GGT | GAC | TGT | CCC | AAC | TTT | GCG | GCT | CCC | CGC | AGA | GAG | GTG | GCA | | | |
| 1116 | | | 1125 | | | 1134 | | | 1143 | | | 1152 | | | | | |
| Pro | Pro | Tyr | 290 | Gln | Gly | Ala | Asp | Pro | 295 | Ile | Leu | Ala | Thr | Ala | Leu | 300 | Ala |
| CCA | CCC | TAT | CAG | GGG | GCT | GAC | CCC | ATC | CTT | GCG | ACA | GCC | CTC | GCC | | | |
| 1161 | | | 1170 | | | 1179 | | | 1188 | | | 1197 | | | | | |
| Ser | Asp | Pro | 305 | Ile | Pro | Asn | Pro | Leu | 310 | Gln | Lys | Trp | Glu | Asp | Ser | 315 | Ala |
| TCC | GAC | CCC | ATC | CCC | AAC | CCC | CTT | CAG | AAG | TGG | GAG | GAC | AGC | GCC | | | |
| 1206 | | | 1215 | | | 1224 | | | 1233 | | | 1242 | | | | | |
| His | Lys | Pro | 320 | Gln | Ser | Leu | Asp | Thr | 325 | Asp | Asp | Pro | Ala | Thr | Leu | 330 | Tyr |
| CAC | AAG | CCA | CAG | AGC | CTA | GAC | ACT | GAT | GAC | CCC | GCG | ACG | CTG | TAC | | | |
| 1251 | | | 1260 | | | 1269 | | | 1278 | | | 1287 | | | | | |
| Ala | Val | Val | 335 | Glu | Asn | Val | Pro | Pro | 340 | Leu | Arg | Trp | | | | | |
| GCC | GTG | GTG | GAG | AAC | GTG | CCC | CCG | TTG | CGC | TGG | AA | <u>GGAATTC</u> | | | | | |
| 1296 | | | 1305 | | | 1314 | | | 1323 | | | 1332 | | | | | |

FIG. 2

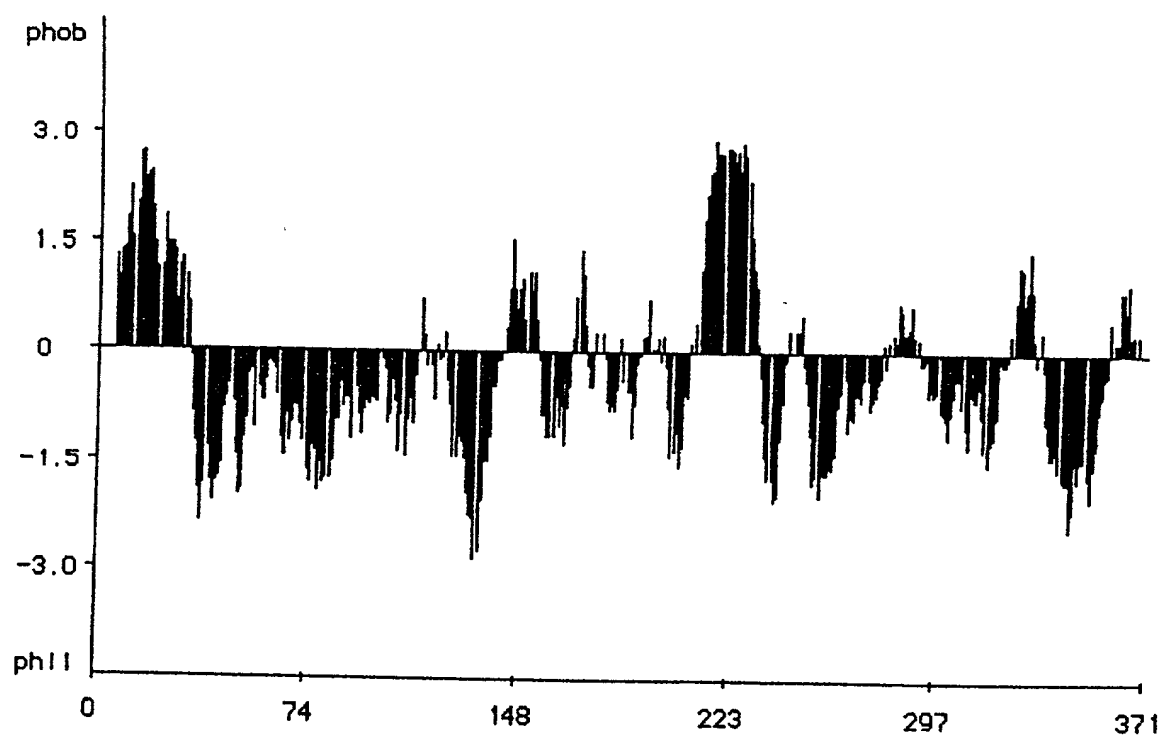


FIG. 3A

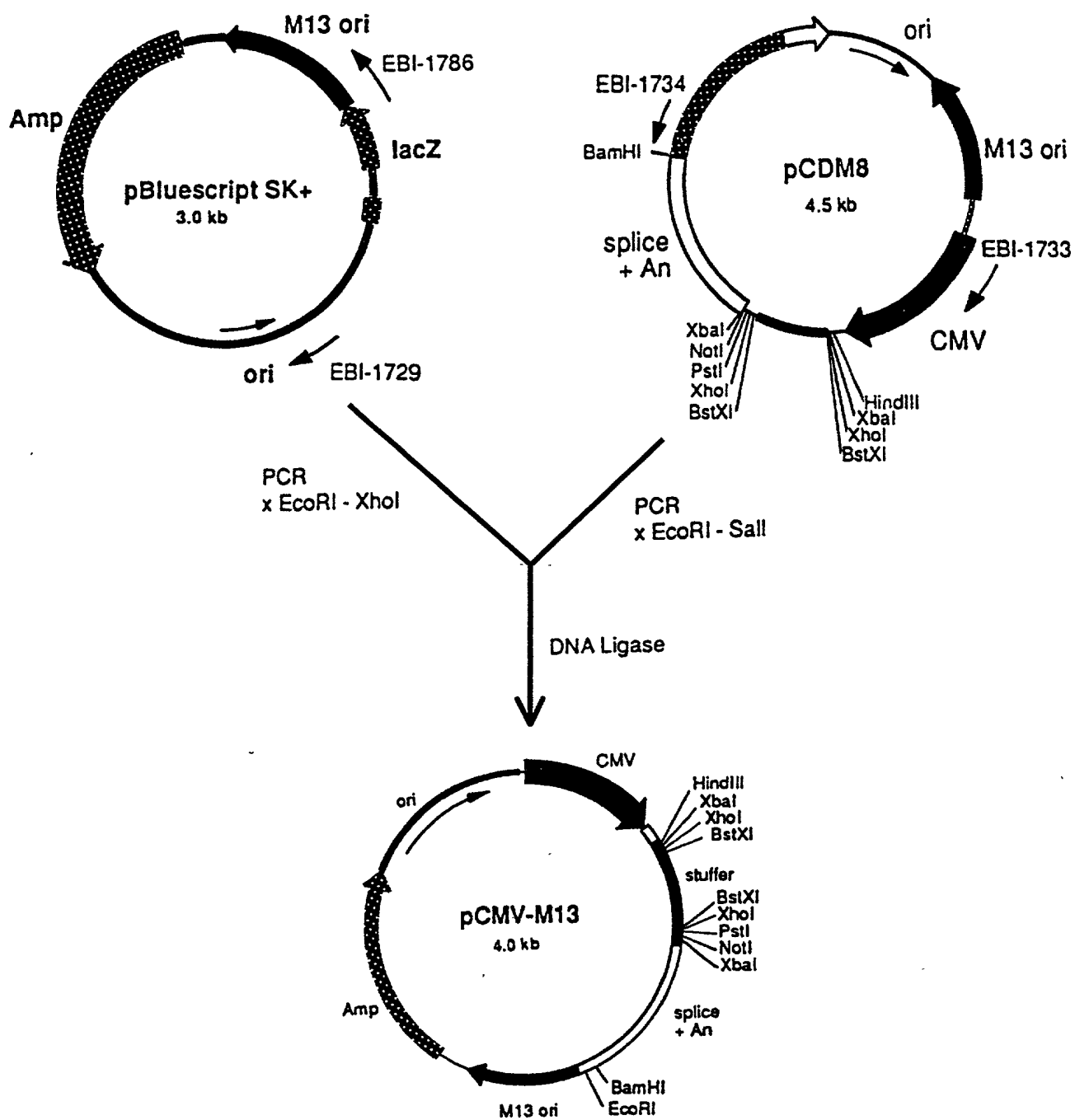


FIG. 3B

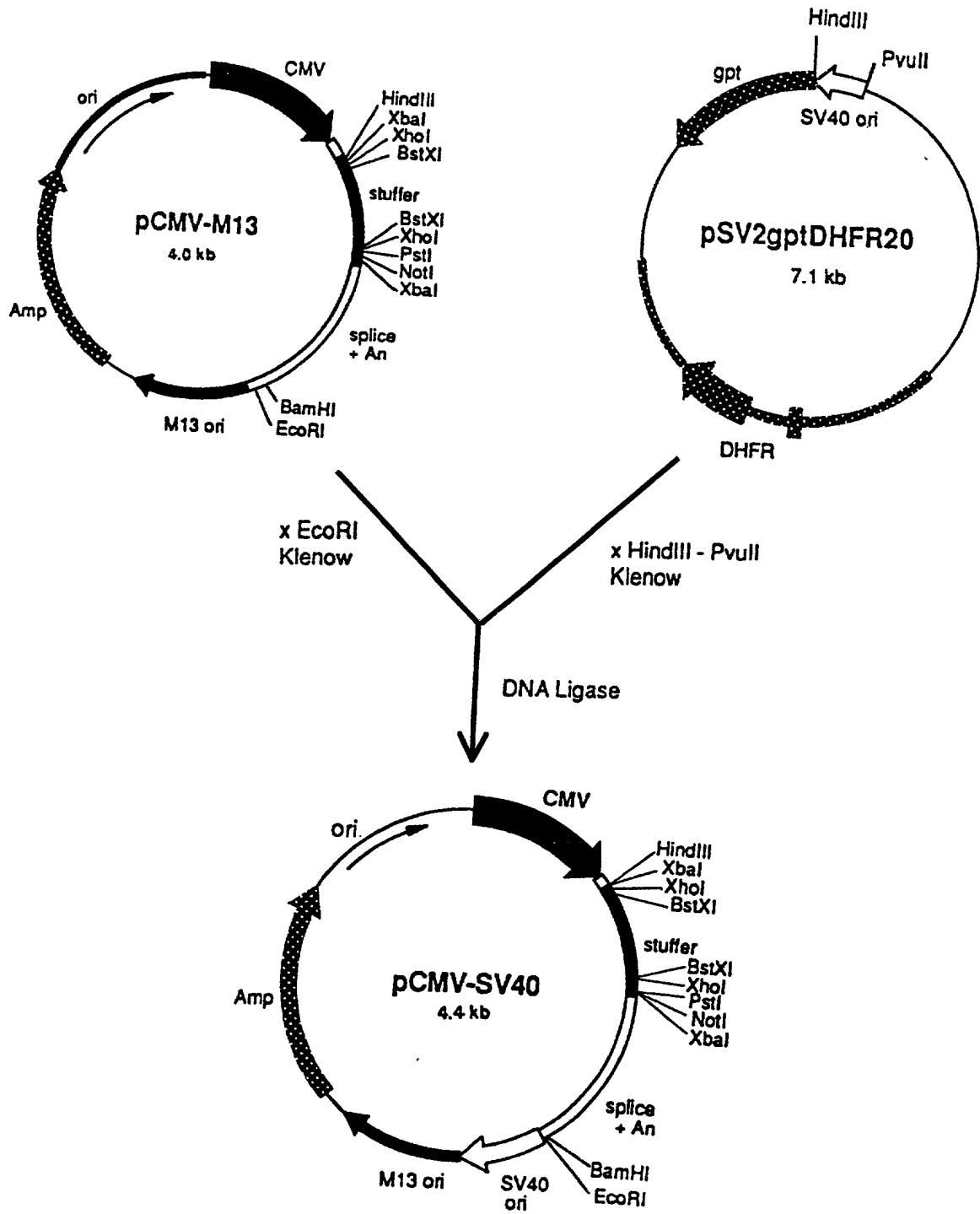


FIG. 4A

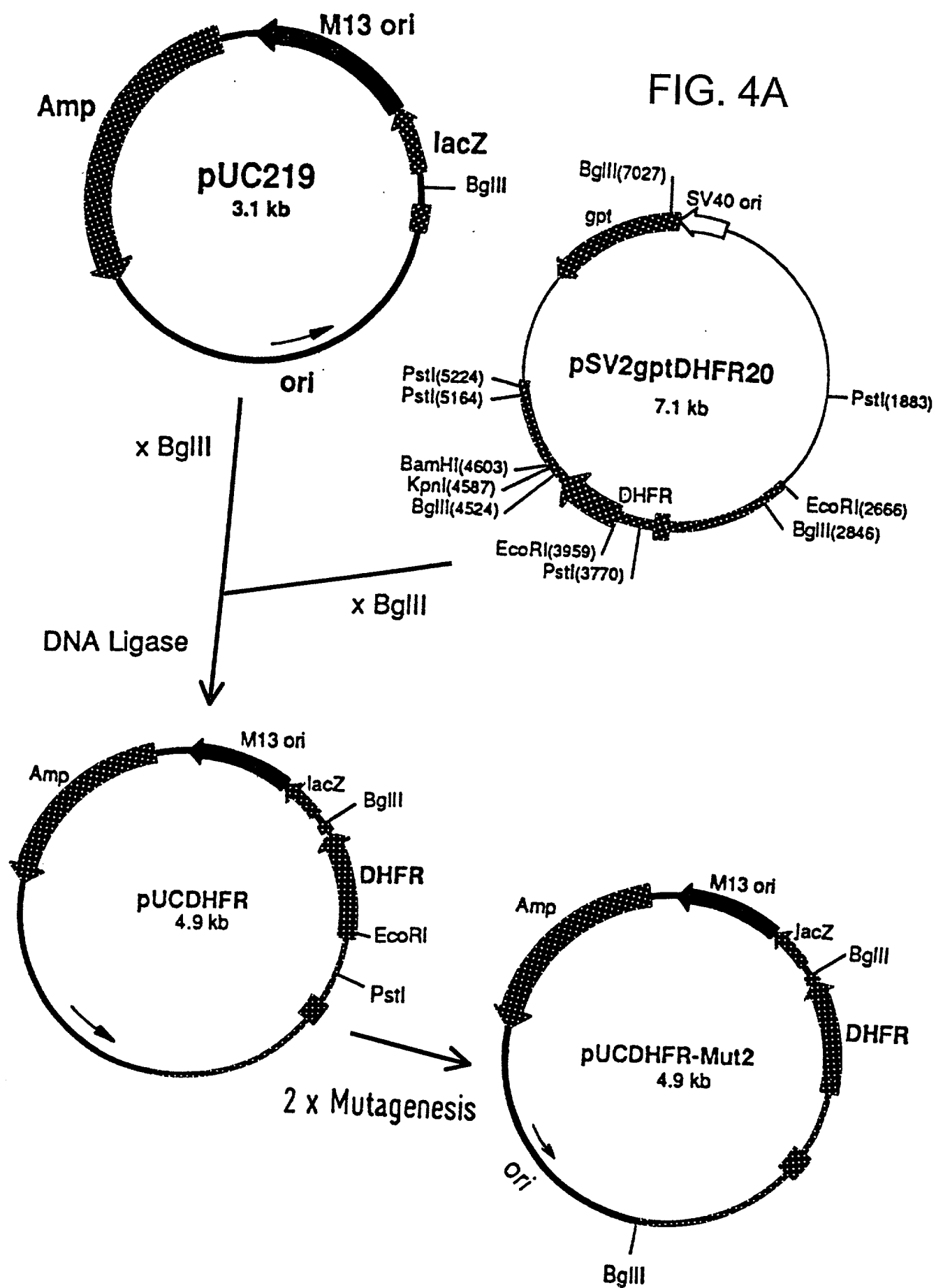
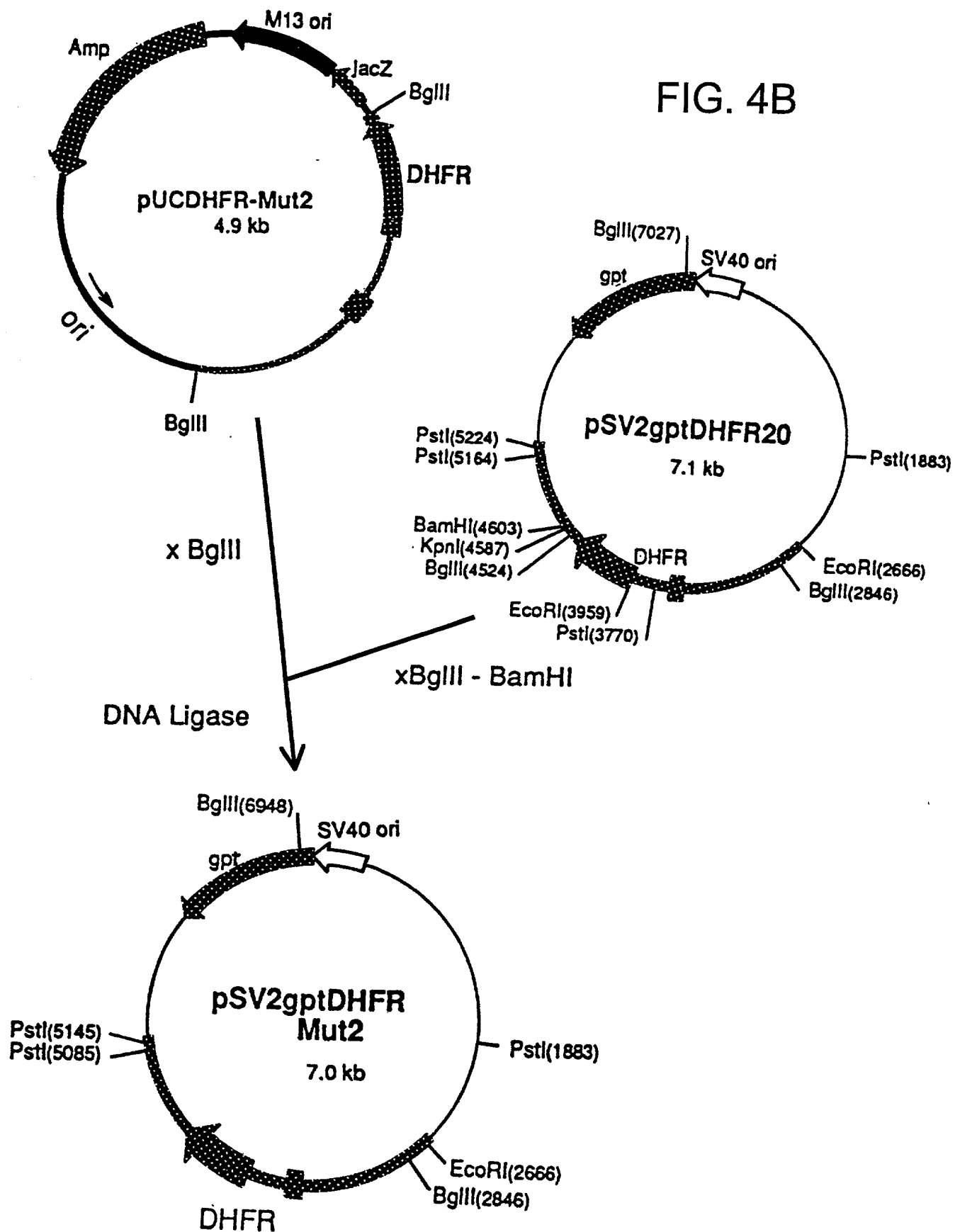


FIG. 4B



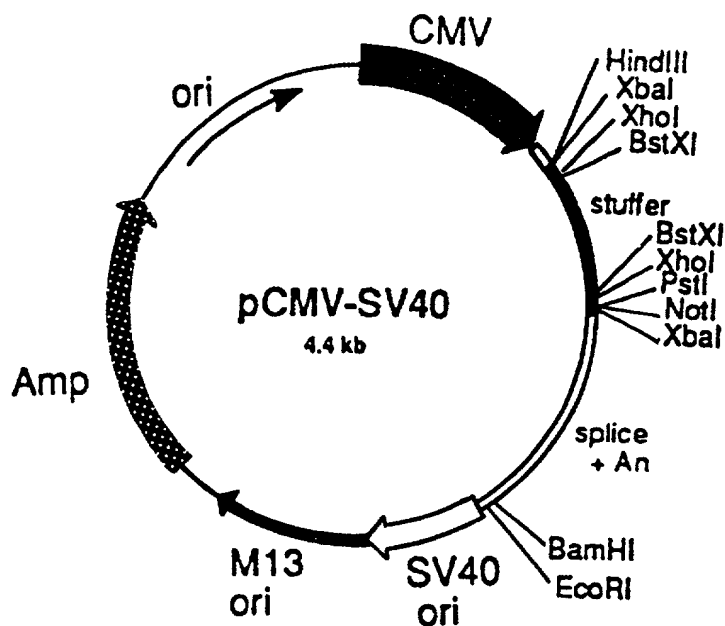
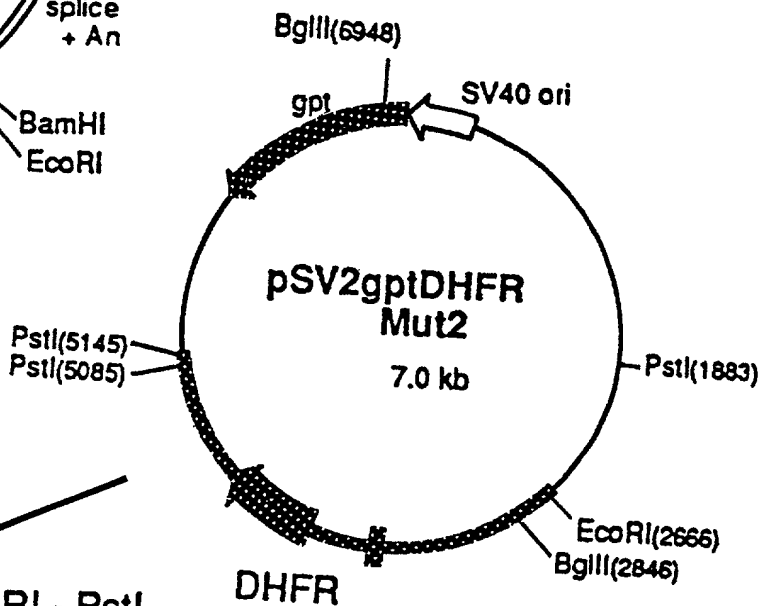


FIG. 5A

x BamHI - EcoRI
Klenow



x EcoRI - PstI
T4 DNA Polymerase

DNA Ligase

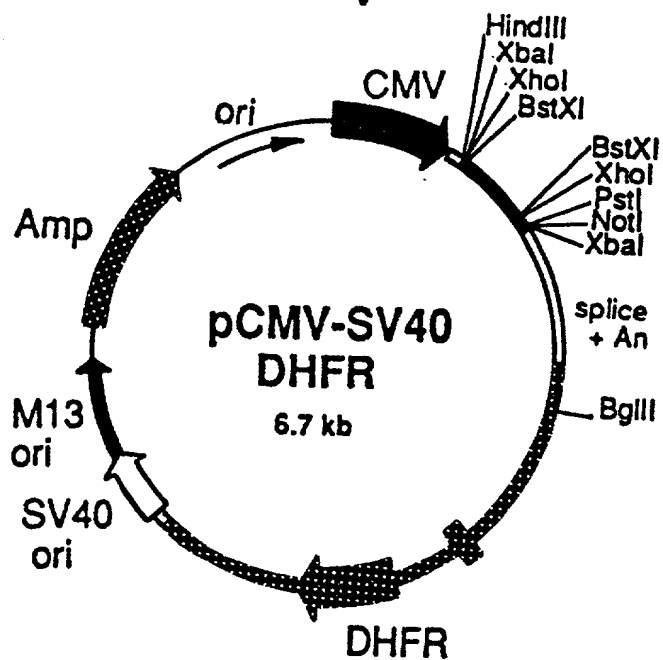


FIG. 5B

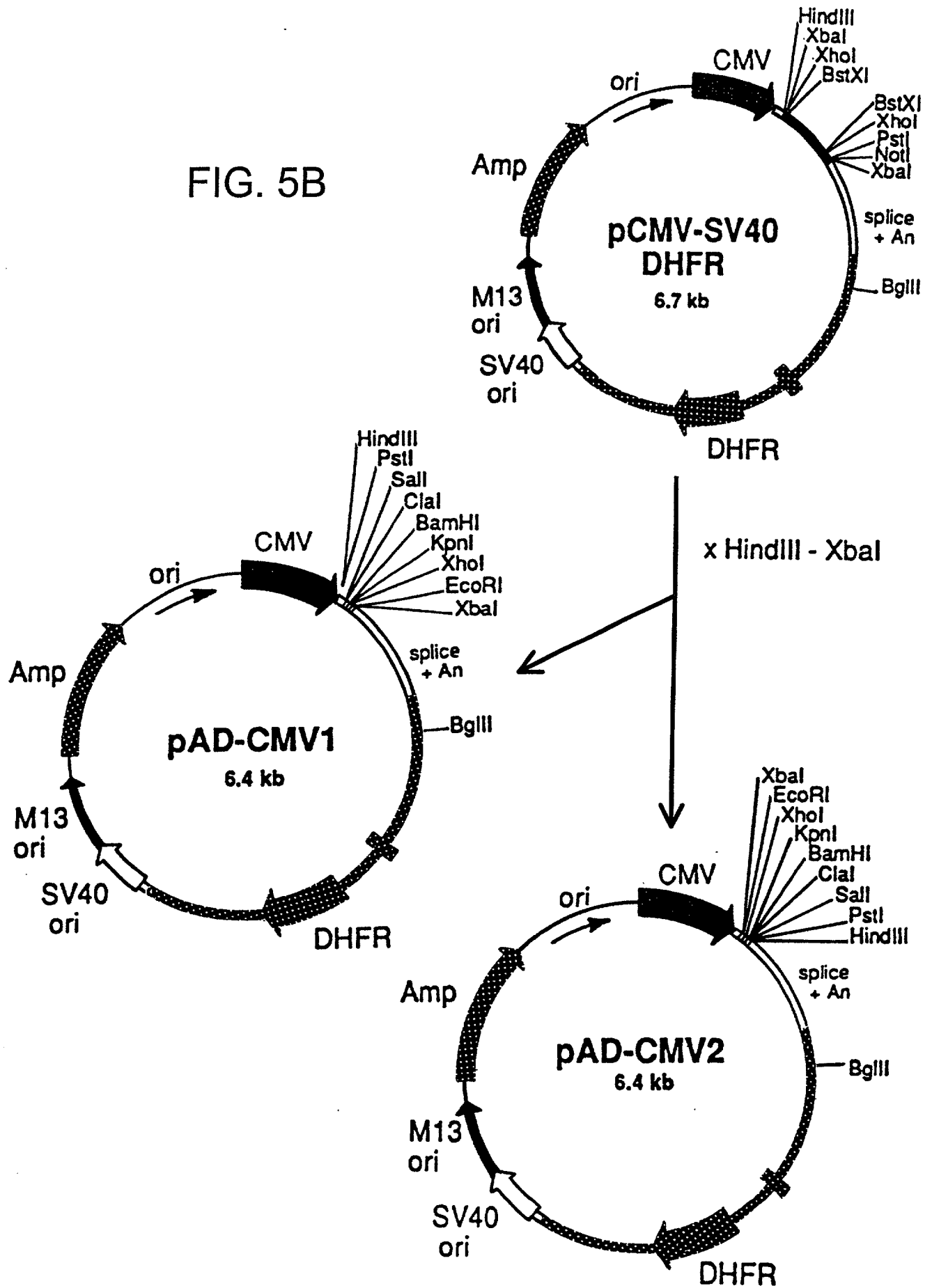


FIG. 6B

ACAGCTTTGT TCTAGTCAGC CAGGCAAGCA TATGTAAATA AAGTCCTCA GGGAAC TGAG 1500

GTTAAAAGAT GTATCCTGGA CCTGCCAGAC CTGGCCATTC ACGTAAACAG AAGATTCCGC 1560

CTCAAGTTCC GGTTAACAAC AGGAGGCAAC GAGATCTCAA ATCTATTACT TCTAATCGGG 1620

TAATTAAAAC CTTTCAACTA AAACACGGAC CCACGGATGT CACCCACTTT TCCTTCCCCG 1680

GCTCCGCCCT TCTCAGTACT CCCACCAT T AGGCTCGCTA CTCCACCTCC ACTTCCGGGC 1740

GCGACACCCA CGTGCCCTCT CCCACCCGAC GCTAACCCCG CCCCTGCCCG TCTGACCCCG 1800

CCCACCACCT GGCCCCGCCC CGTTGAGGAC AGAAGAAACC CCGGGCAGCC GCAGCCAAGG 1860

CGGACGGGTA GACGCTGGGG GCGCTGAGGA GTCGTCCTCT ACCTTCTCTG CTGGCTCGGT 1920

GGGGGACGCG GTGGATCTCA GGCTTCCGGA AGACTGGAAG AACCGGCTCA GAACCGCTTG 1980

TCTCCGCGGG GCTTGGGCGG CGGAAGAATG GCCGCTAGAC GCGGACTTGG TCGAGGCAT 2040

CGCAGGATGC AGAAGAGCAA GCCCGCCGGG AGCGCGCGGC TG TACTACCC CGCGCCTGGA 2100

GCGGCCACGC CGGACTGGGC GGGGCCGGCC TGGTGGAGGC GGAGTCTGAC CTCGTGGAGG 2160

CGGGGCCTCT GATGTTCAA TAGGATGCTA GGCTTGTTGA GCGTGGCCT CCGATTCACA 2220

AGTGGGAAGC AGCGCCGGGC GACTGCAATT TCGCGCCAAA CTTGGGGGAA GCACAGCGTA 2280

CAGGCTGCCT AGGTGATCGC TGCTGCTGTC ATGGTTCGAC CGCTGAACTG CATCGTCGCC 2340

GTGTCCCAGA ATATGGGCAT CGGCAAGAAC GGAGACCTTC CCTGGCCAAT GCTCAGGTAC 2400

TGGCTGGATT GGGTTAGGGA AACCGAGGCG GTTCGCTGAA TCGGGTCGAG CACTTGGCGG 2460

AGACGCGCGG GCCAACTACT TAGGGACAGT CATGAGGGGT AGGCCCCGCC GCTGCTGCCC 2520

TTGCCCATGC CCGCGGTGAT CCCCATGCTG TGCCAGCCTT TGCCCAGAGG CGCTCTAGCT 2580

GGGAGCAAAG TCCGGTCACT GGGCAGCACC ACCCCCCGGA CTTGCATGGG TAGCCGCTGA 2640

GATGGAGCCT GAGCACACGT GACAGGGTCC CTGTTAACGC AGTGTTTCTC TAACTTTCAG 2700

GAACGAGTTC AAGTACTTCC AAAGAATGAC CACCACCTCC TCAGTGGAAG GTAAACAGAA 2760

CCTGGTGATT ATGGGCCGGA AAACCTGGTT CTCCATTCCT GAGAAGAATC GACCTTTAAA 2820

GGACAGAATT AATATAGTTC TCAGTAGAGA GCTCAAGGAA CCACCACAAG GAGCTCATTT 2880

TCTTGCCAAA AGTCTGGACC ATGCCTTAAA ACTTATTGAA CAACCAGAGT TAGCAGATAA 2940

AGTGGACATG GTTTGGATAG TTGGAGGCAG TTCCGTTTAC AAGGAAGCCA TGAATCAGCC 3000

CGCGCTAGAC

FIG. 6C

| | |
|--|------|
| AGGCCATCTC AGACTCTTTG TGACAAGGAT CATGCAGGAA TTTGAAAGTG ACACGTTCTT | 3060 |
| CCCAGAAATT GATTTGGAGA AATATAAACT TCTCCCAGAG TACCCAGGGG TCCTTTCTGA | 3120 |
| AGTCCAGGAG GAAAAAGGCA TCAAGTATAA ATTTGAAGTC TATGAGAAGA AAGGCTAACA | 3180 |
| GAAAGATACT TGCTGATTGA CTTCAAGTTC TACTGCTTTC CTCCTAAAAT TATGCATTTT | 3240 |
| TACAAGACCA TGGGACTTGT GTTGGCTTTA GATCCTGTGC ATCCTGGGCA ACTGTTGTAC | 3300 |
| TCTAAGCCAC TCCCCAAAGT CATGCCCCAG CCCCTGTATA ATTCTAAACA ATTAGAATTA | 3360 |
| TTTTCATTTT CATTAGTCTA ACCAGGTTAT ATTAAATATA CTTTAAGAAA CACCATTGTC | 3420 |
| CATAAAGTTC TCAATGCCCC TCCCATGCAG CCTCAAGTGG CTCCCCAGCA GATGCATAGG | 3480 |
| GTAGTGTGTG TACAAGAGAC CCCAAAGACA TAGAGCCCCT GAGAGCATGA GCTGATATGG | 3540 |
| GGGCTCATAG AGATAGGAGC TAGATGAATA AGTACAAAGG GCAGAAATGG GTTTTAACCA | 3600 |
| GCAGAGCTAG AACTCAGACT TTAAAGAAAA TTAGATCAAA GTAGAGACTG AATTATTCTG | 3660 |
| CACATCAGAC TCTGAGCAGA GTTCTGTTCA CTCAGACAGA AAATGGGTAA ATTGAGAGCT | 3720 |
| GGCTCCATTG TGCTCCTTAG AGATGGGAGC AGGTGGAGGA TTATATAAGG TCTGGAACAT | 3780 |
| TTAACTTCTC CGTTTCTCAT CTTCAAGTGG ATTCCAAGGG ATACTACAAT TCTGTGGAAT | 3840 |
| GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG CAGGCAGAAG TATGCAAAGC | 3900 |
| ATGCATCTCA ATTAGTCAGC AACCAGGTGT GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA | 3960 |
| AGTATGCAAA GCATGCATCT CAATTAGTCA GCAACCATAG TCCCGCCCCCT AACTCCGCCC | 4020 |
| ATCCCGCCCC TAACTCCGCC CAGTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT | 4080 |
| TTTATTTATG CAGAGGCCGA GGCGCCTCTG AGCTATTCCA GAAGTAGTGA GGAGGCTTTT | 4140 |
| TTGGAGGCCT AGGCTTTTGC AAAAAAGCTA ATTCAGCCTG AATGGCGAAT GGGACGCGCC | 4200 |
| CTGTAGCGGC GCATTAAGCG CGGCGGGTGT GGTGGTTACG CGCAGCGTGA CCGCTACACT | 4260 |
| TGCCAGCGCC CTAGCGCCCC CTCCTTTCGC TTTCTTCCCT TCCTTTCTCG CCACGTTTCG | 4320 |
| CGGCTTTCCC CGTCAAGCTC TAAATCGGGG GCTCCCTTTA GGGTTCCGAT TTAGTGCTTT | 4380 |
| ACGGCACCTC GACCCCAAAA ACTTGATTAG GGTGATGGTT CACGTAGTGG GCCATCGCCC | 4440 |
| TGATAGACGG TTTTTCGCCC TTTGACGTTG GAGTCCACGT TCTTTAATAG TGGACTCTTG | 4500 |
| TTCCAAACTG GAACAACACT CAACCCTATC TCGGTCTATT CTTTGTATTT ATAAGGGATT | 4560 |

FIG. 6D

| | |
|--|------|
| TTGCCGATTT CGGCCTATTG GTAAAAAAT GAGCTGATTT AACAAAAATT TAACGCGAAT | 4620 |
| TTTAACAAAA TATTAACGTT TACAATTTCA GGTGGCACTT TTCGGGGAAA TGTGCGCGGA | 4680 |
| ACCCCTATTT GTTTATTTTT CTAAATACAT TCAAATATGT ATCCGCTCAT GAGACAATAA | 4740 |
| CCCTGATAAA TGCTTCAATA ATATTGAAA AGGAAGAGTA TGAGTATTCA ACATTTCCTG | 4800 |
| GTCGCCCTTA TTCCCTTTTT TCGGCATTT TGCCTTCCTG TTTTGCTCA CCCAGAAACG | 4860 |
| CTGGTGAAAG TAAAAGATGC TGAAGATCAG TTGGGTGCAC GAGTGGGTTA CATCGAACTG | 4920 |
| GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTCGCCCCG AAGAACGTTT TCCAATGATG | 4980 |
| AGCACTTTTA AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTATTGACGC CGGGCAAGAG | 5040 |
| CAACTCGGTC GCCGCATACA CTATTCTCAG AATGACTTGG TTGAGTACTC ACCAGTCACA | 5100 |
| GAAAAGCATC TTACGGATGG CATGACAGTA AGAGAATTAT GCAGTGCTGC CATAACCATG | 5160 |
| AGTGATAACA CTGCGGCCAA CTTACTTCTG ACAACGATCG GAGGACCGAA GGAGCTAACC | 5220 |
| GCTTTTTTGC ACAACATGGG GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG | 5280 |
| AATGAAGCCA TACCAAACGA CGAGCGTGAC ACCACGATGC CTGTAGCAAT GGCAACAACG | 5340 |
| TTGCGCAAAC TATTAAGTGG CGAACTACTT ACTCTAGCTT CCCGGCAACA ATTAATAGAC | 5400 |
| TGGATGGAGG' CGGATAAAGT TGCAGGACCA CTTCTGCGCT CGGCCCTTCC GGCTGGCTGG | 5460 |
| TTTATTGCTG ATAAATCTGG AGCCGGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG | 5520 |
| GGGCCAGATG GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT | 5580 |
| ATGGATGAAC GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTGGTAA | 5640 |
| CTGTCAGACC AAGTTTACTC ATATATACTT TAGATTGATT TAAAACTTCA TTTTAAATTT | 5700 |
| AAAAGGATCT AGGTGAAGAT CCTTTTTGAT AATCTCATGA CCAAAATCCC TTAACGTGAG | 5760 |
| TTTTCGTTCC ACTGAGCGTC AGACCCCGTA GAAAAGATCA AAGGATCTTC TTGAGATCCT | 5820 |
| TTTTTTCTGC GCGTAATCTG CTGCTTGCAA ACAAAAAAAC CACCGCTACC AGCGGTGGTT | 5880 |
| TGTTTGCCGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG | 5940 |
| CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG GCCACCACTT CAAGAACTCT | 6000 |
| GTAGCACCGC CTACATACCT CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC | 6060 |
| GATAAGTCGT GTCTTACCGG GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG | 6120 |

FIG. 6E

TCGGGCTGAA CGGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA 6180
CTGAGATACC TACAGCGTGA GCATTGAGAA AGCGCCACGC TTCCCGAAGG GAGAAAGGCG 6240
GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGA GCTTCCAGGG 6300
GGAAACGCCT GGTATCTTTA TAGTCCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA 6360
TTTTTGTGAT GCTCGTCAGG GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCC

6180 6240 6300 6360

FIG. 7A

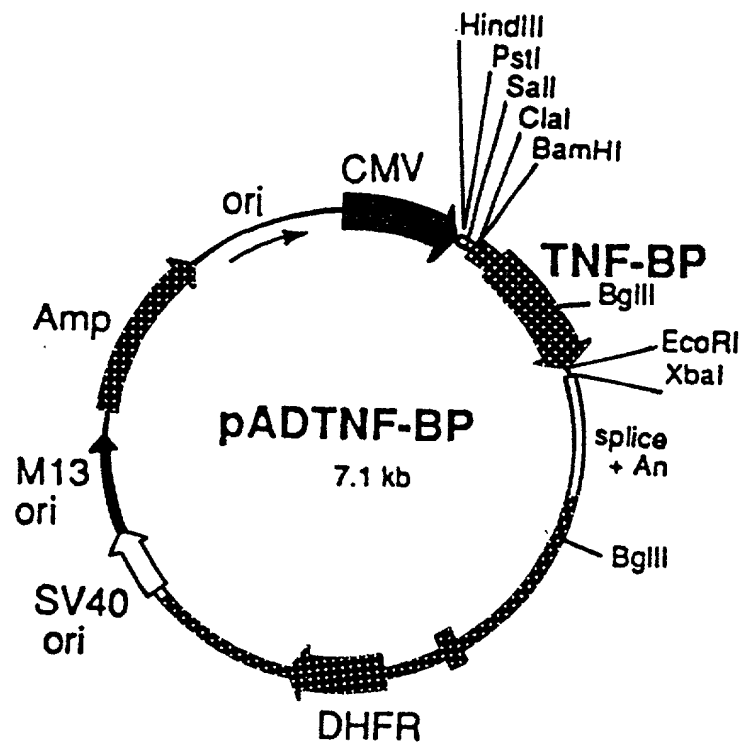


FIG. 7B

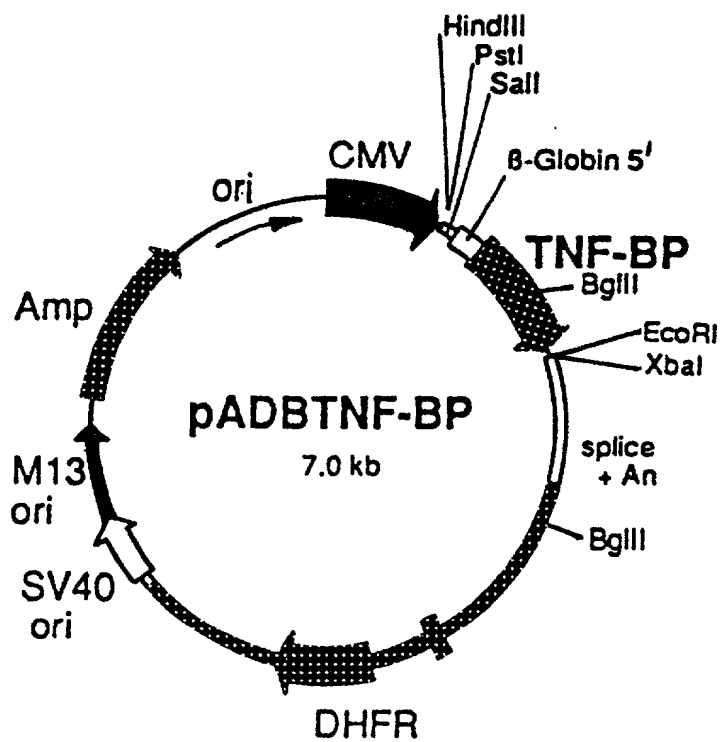


FIG. 7C

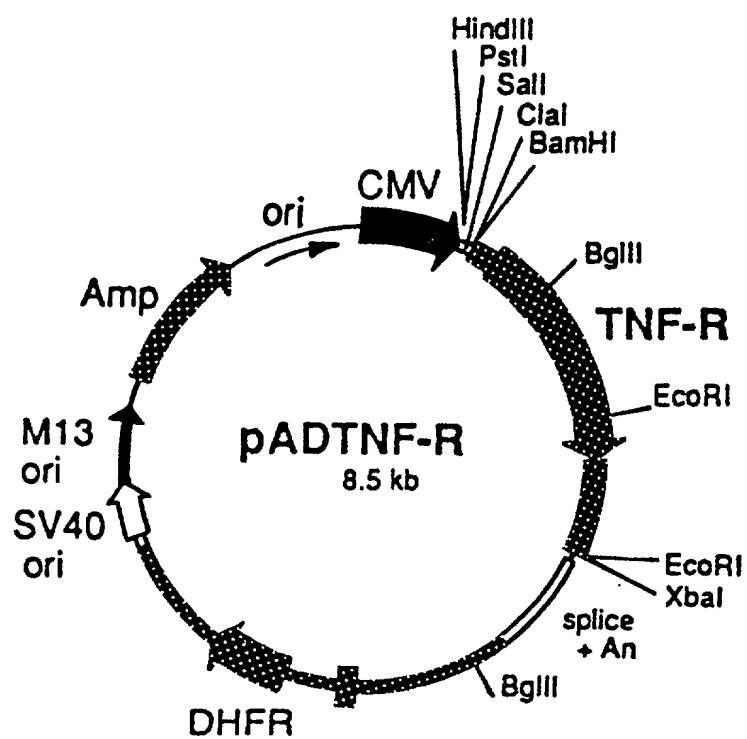


FIG. 7D

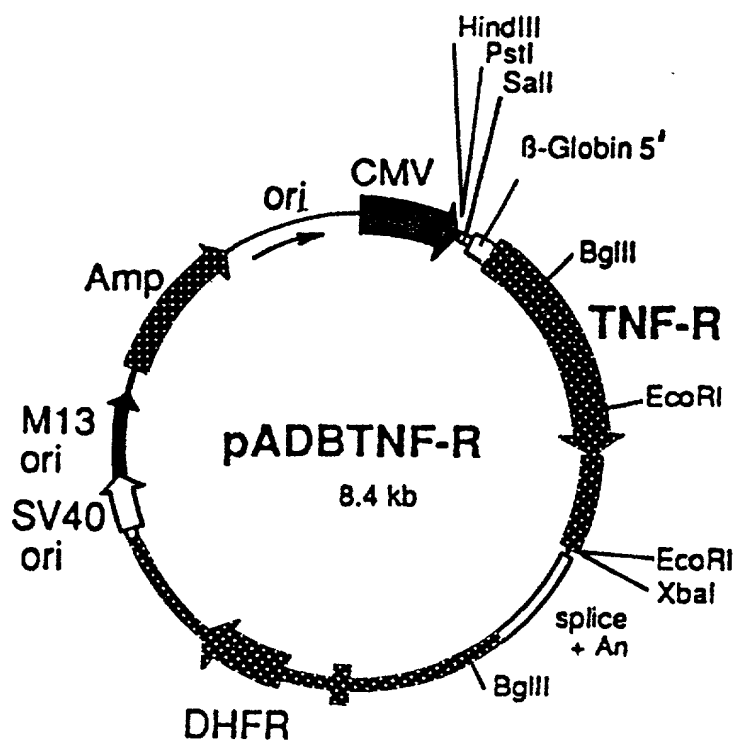


FIG. 8A

raTNF-R

| | | | | | | |
|---|------------|------------|------------|------------|------------|-----|
| GAATTCCTTT | TCTCCGAGTT | TTCTGAACTC | TGGCTCATGA | TCGGGCTTAC | TGGATACGAG | 60 |
| AATCCTGGAG, | GACCGTACCC | TGATTTCCAT | CTACCTCTGA | CTTTGAGCCT | TTCTAACCCG | 120 |
| GGGCTCACGC | TGCCAACACC | CGGGCCACCT | GGTCCGATCG | TCTTACTTCA | TTCACCAGCG | 180 |
| TTGCCAATTG | CTGCCCTGTC | CCCAGCCCCA | ATGGGGGAGT | GAGAGAGGCC | ACTGCCGGCC | 240 |
| GGAC | | | | | | |
| 245/1 | | | | 275/11 | | |
| ATG GGT CTC CCC ATC GTG CCT GGC CTG CTG CTG TCA CTG GTG CTC CTG GCT CTG CTG ATG | | | | | | |
| Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu Leu Ala Leu Leu Met | | | | | | |
| 305/21 | | | | 335/31 | | |
| GGG ATA CAC CCA TCA GGG GTC ACC GGA CTG GTT CCT TCT CTT GGT GAC CGG GAG AAG AGG | | | | | | |
| Gly Ile His Pro Ser Gly Val Thr Gly Leu Val Pro Ser Leu Gly Asp Arg Glu Lys Arg | | | | | | |
| 365/41 | | | | 395/51 | | |
| GAT AAT TTG TGT CCC CAG GGA AAG TAT GCC CAT CCA AAG AAT AAT TCC ATC TGC TGC ACC | | | | | | |
| Asp Asn Leu Cys Pro Gln Gly Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr | | | | | | |
| 425/61 | | | | 455/71 | | |
| AAG TGC CAC AAA GGA ACC TAC TTG GTG AGT GAC TGT CCA AGC CCA GGG CAG GAA ACA GTC | | | | | | |
| Lys Cys His Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr Val | | | | | | |
| 485/81 | | | | 515/91 | | |
| TGC GAG CTC TCT CAT AAA GGC ACC TTT ACA GCT TCG CAG AAC CAC GTC AGA CAG TGT CTC | | | | | | |
| Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His Val Arg Gln Cys Leu | | | | | | |
| 545/101 | | | | 575/111 | | |
| AGT TGC AAG ACA TGT CGG AAA GAA ATG TTC CAG GTG GAG ATT TCT CCT TGC AAA GCT GAC | | | | | | |
| Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln Val Glu Ile Ser Pro Cys Lys Ala Asp | | | | | | |
| 605/121 | | | | 635/131 | | |
| ATG GAC ACC GTG TGT GGC TGC AAG AAG AAC CAA TTC CAG CGC TAC CTG AGT GAG ACG CAT | | | | | | |
| Met Asp Thr Val Cys Gly Cys Lys Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His | | | | | | |
| 665/141 | | | | 695/151 | | |
| TTC CAG TGT GTG GAC TGC AGC CCC TGC TTC AAT GGC ACC GTG ACA ATC CCC TGT AAG GAG | | | | | | |
| Phe Gln Cys Val Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys Glu | | | | | | |
| 725/161 | | | | 755/171 | | |
| AAA CAG AAC ACC GTG TGT AAC TGC CAC GCA GGA TTC TTT CTA AGC GGA AAT GAG TGC ACC | | | | | | |
| Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser Gly Asn Glu Cys Thr | | | | | | |
| 785/181 | | | | 815/191 | | |
| CCT TGC AGC CAC TGC AAG AAA AAT CAG GAA TGT ATG AAG CTG TGC CTA CCT CCA GTT GCA | | | | | | |
| Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys Met Lys Leu Cys Leu Pro Pro Val Ala | | | | | | |
| 845/201 | | | | 875/211 | | |
| AAT GTC ACA AAC CCC CAG GAC TCA GGT ACT GCC GTG CTG TTG CCT CTG GTT ATC TTC CTA | | | | | | |
| Asn Val Thr Asn Pro Gln Asp Ser Gly Thr Ala Val Leu Leu Pro Leu Val Ile Phe Leu | | | | | | |
| 905/221 | | | | 935/231 | | |
| GGT CTT TGC CTT TTA TTC TTT ATC TGC ATC AGT CTA CTG TGC CGA TAT CCC CAG TGG AGG | | | | | | |
| Gly Leu Cys Leu Leu Phe Phe Ile Cys Ile Ser Leu Leu Cys Arg Tyr Pro Gln Trp Arg | | | | | | |
| 965/241 | | | | 995/251 | | |
| CCC AGG GTC TAC TCC ATC ATT TGT AGG GAT TCA GCT CCT GTC AAA GAG GTG GAG GGT GAA | | | | | | |
| Pro Arg Val Tyr Ser Ile Ile Cys Arg Asp Ser Ala Pro Val Lys Glu Val Glu Gly Glu | | | | | | |
| 1025/261 | | | | 1055/271 | | |
| GGA ATT GTT ACT AAG CCC CTA ACT CCA GCC TCT ATC CCA GCC TTC AGC CCC AAC CCC GGC | | | | | | |
| Gly Ile Val Thr Lys Pro Leu Thr Pro Ala Ser Ile Pro Ala Phe Ser Pro Asn Pro Gly | | | | | | |
| 1085/281 | | | | 1115/291 | | |
| TTC AAC CCC ACT CTG GGC TTC AGC ACC ACC CCA CGC TTC AGT CAT CCT GTC TCC AGT ACC | | | | | | |
| Phe Asn Pro Thr Leu Gly Phe Ser Thr Thr Pro Arg Phe Ser His Pro Val Ser Ser Thr | | | | | | |
| 1145/301 | | | | 1175/311 | | |
| CCC ATC AGC CCC GTC TTC GGT CCT AGT AAC TGG CAC AAC TTC GTG CCA CCT GTA AGA GAG | | | | | | |
| Pro Ile Ser Pro Val Phe Gly Pro Ser Asn Trp His Asn Phe Val Pro Pro Val Arg Glu | | | | | | |
| 1205/321 | | | | 1235/331 | | |
| GTG GTC CCA ACC CAG GGT GCT GAC CCT CTC CTC TAC GGA TCC CTC AAC CCT GTG CCA ATC | | | | | | |
| Val Val Pro Thr Gln Gly Ala Asp Pro Leu Leu Tyr Gly Ser Leu Asn Pro Val Pro Ile | | | | | | |

FIG. 8A

FIG. 8B

1265/341 1295/351
CCC GCC CCT GTT CGG AAA TGG GAA GAC GTC GTC GCG GCC CAG CCA CAA CGG CTT GAC ACT
Pro Ala Pro Val Arg Lys Trp Glu Asp Val Val Ala Ala Gln Pro Gln Arg Leu Asp Thr
1325/361 1355/371
GCA GAC CCT GCG ATG CTG TAT GCT GTG GTG GAT GGC GTG CCT CCG ACA CGC TGG AAG GAG
Ala Asp Pro Ala Met Leu Tyr Ala Val Val Asp Gly Val Pro Pro Thr Arg Trp Lys Glu
1385/381 1415/391
TTC ATG CGG CTC CTG GGG CTG AGC GAG CAC GAG ATC GAG CGG CTG GAG CTG CAG AAC GGG
Phe Met Arg Leu Leu Gly Leu Ser Glu His Glu Ile Glu Arg Leu Glu Leu Gln Asn Gly
1445/401 1475/411
CGT TGC CTC CGC GAG GCT CAT TAC AGC ATG CTG GAA GCC TGG CGG CGC CGC ACA CCG CGA
Arg Cys Leu Arg Glu Ala His Tyr Ser Met Leu Glu Ala Trp Arg Arg Arg Thr Pro Arg
1505/421 1535/431
CAC GAG GCC ACG CTG GAC GTA GTG GGC CGC GTG CTT TGC GAC ATG AAC CTG CGT GGC TGC
His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu Cys Asp Met Asn Leu Arg Gly Cys
1565/441 1595/451
CTG GAG AAC ATC CGC GAG ACT CTA GAA AGC CCT GCC CAC TCG TCC ACG ACC CAC CTC CCG
Leu Glu Asn Ile Arg Glu Thr Leu Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro
1625/461
CGA TAA
Arg Stop

GGCCACACCC CCACCTCAGG AACGGGACTC GAAGGACCAT CCTGCTAGAT 1680
GCCCTGCTTC CCTGTGAACC TCCTCTTTGG TCCTCTAGGG GGCAGGCTCG ATCTGGCAGG 1740
CTCGATCTGG CAGCCACTTC CTTGGTGCTA CCGACTTGGT GTACATAGCT TTTCCCAGCT 1800
GCCGAGGACA GCCTGTGCCA GCCACTTG TG CATGGCAGGG AAGTGTGCCA TCTGCTCCCA 1860
GACAGCTGAG GGTGCCAAAA GCCAGGAGAG GTGATTGTGG AGAAAAAGCA CAATCTATCT 1920
GATACCCACT TGGGATGCAA GGACCCAAAC AAAGCTTCTC AGGGCCTCCT CAGTTGATTT 1980
CTGGGGCCCTT TTCACAGTAG ATAAAACAGT CTTTGTATTG ATTATATCAC ACTAATGGAT 2040
GAACGGTTGA ACTCCCTAAG GTAGGGGCAA GCACAGAACA GTGGGGTCTC CAGCTGGAGC 2100
CCCCGACTCT TGTAATACA CTAAAAATCT AAAAGTGAAA AAAAAAAAAA AAAAAAAAAA 2160
AAAAAAGGAA TTC

FIG. 9A

huTNF-R

GAATTCCTCTG GACTGAGGCT CCAGTTCTGG CCTTTGGGGT TCAAGATCAC TGGGACCAGG 60
CCGTGATCTC TATGCCCCGAG TCTCAACCTT CAACTGTCAC CCCAAGGCAC TTGGGACGTC 120
CTGGACAGAC CGAGTCCCCG GAAGCCCCAG CACTGCCGCT GCCACACTGC CCTGAGCCCA 180
AATGGGGGAG TGAGAGGCCA TAGCTGTCTG GC

213/1

ATG GGC CTC TCC ACC GTG CCT GAC CTG CTG CTG CCA CTG GTG CTC CTG GAG CTG TTG GTG
Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val
273/21

GGA ATA TAC CCC TCA GGG GTT ATT GGA CTG GTC CCT CAC CTA GGG GAC AGG GAG AAG AGA
Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg
333/41

GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG ATT TGC TGT ACC
Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr
393/61

AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT CCA GGC CCG GGG CAG GAT ACG GAC
Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
453/81

TGC AGG GAG TGT GAG AGC GGC TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC
Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu
513/101

AGC TGC TCC AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC
Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
573/121

CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG AGT GAA AAC CTT
Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu
633/141

TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT GGG ACC GTG CAC CTC TCC TGC CAG GAG
Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
693/161

AAA CAG AAC ACC GTG TGC ACC TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC
Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val
753/181

TCC TGT AGT AAC TGT AAG AAA AGC CTG GAG TGC ACG AAG TTG TGC CTA CCC CAG ATT GAG
Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
813/201

AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC ACA GTG CTG TTG CCC CTG GTC ATT TTC TTT
Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe
873/221

GGT CTT TGC CTT TTA TCC CTC CTC TTC ATT GGT TTA ATG TAT CGC TAC CAA CGG TGG AAG
Gly Leu Cys Leu Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
933/241

TCC AAG CTC TAC TCC ATT GTT TGT GGG AAA TCG ACA CCT GAA AAA GAG GGG GAG CTT GAA
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu Gly Glu Leu Glu
993/261

GGA ACT ACT ACT AAG CCC CTG GCC CCA AAC CCA AGC TTC AGT CCC ACT CCA GGC TTC ACC
Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser Phe Ser Pro Thr Pro Gly Phe Thr
1053/281

CCC ACC CTG GGC TTC AGT CCC GTG CCC AGT TCC ACC TTC ACC TCC AGC TCC ACC TAT ACC
Pro Thr Leu Gly Phe Ser Pro Val Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr
1113/301

CCC GGT GAC TGT CCC AAC TTT GCG GCT CCC CGC AGA GAG GTG GCA CCA CCC TAT CAG GGG
Pro Gly Asp Cys Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
1173/321

GCT GAC CCC ATC CTT GCG ACA GCC CTC GCC TCC GAC CCC ATC CCC AAC CCC CTT CAG AAG
Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn Pro Leu Gln Lys

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FIG. 9B

1233/341 1263/351
TGG GAG GAC AGC GCC CAC AAG CCA CAG AGC CTA GAC ACT GAT GAC CCC GCG ACG CTG TAC
Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp Thr Asp Asp Pro Ala Thr Leu Tyr
1293/361 1323/371
GCC GTG GTG GAG AAC GTG CCC CCG TTG CGC TGG AAG GAA TTC GTG CGG CGC CTA GGG CTG
Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu
1353/381 1383/391
AGC GAC CAC GAG ATC GAT CGG CTG GAG CTG CAG AAC GGG CGC TGC CTG CGC GAG GCG CAA
Ser Asp His Glu Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
1413/401 1443/411
TAC AGC ATG CTG GCG ACC TGG AGG CGG CGC ACG CCG CGG CGC GAG GCC ACG CTG GAG CTG
Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu Leu
1473/421 1503/431
CTG GGA CGC GTG CTC CGC GAC ATG GAC CTG CTG GGC TGC CTG GAG GAC ATC GAG GAG GCG
Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu Asp Ile Glu Glu Ala
1533/441 1563/451
CTT TGC GGC CCC GCC GCC CTC CCG CCC GCG CCC AGT CTT CTC AGA TGA 1580
Leu Cys Gly Pro Ala Ala Leu Pro Pro Ala Pro Ser Leu Leu Arg Stop

GGCTGCGCCC CTGCGGGCAG CTCTAAGGAC CGTCCTGCGA 1620
GATCGCCTTC CAACCCCACT TTTTCTGGA AAGGAGGGGT CCTGCAGGGG CAAGCAGGAG 1680
CTAGCAGCCG CCTACTTGGT GCTAACCCCT CGATGTACAT AGCTTTTCTC AGCTGCCTGC 1740
GCGCCGCCGA CAGTCAGCGC TGTGCGCGCG GAGAGAGGTG CGCCGTGGGC TCAAGAGCCT 1800
GAGTGGGTGG TTTGCGAGGA TGAGGGACGC TATGCCTCAT GCCCGTTTGG GGTGTCCTCA 1860
CCAGCAAGGC TGCTCGGGGG CCCCTGGTTC GTCCCTGAGC CTTTTTCACA GTGCATAAGC 1920
AGTTTTTTTT GTTTTGTGTT TGTGTTGTTT TGTTTTTAAA TCAATCATGT TACACTAATA 1980
GAACTTGGC ACTCCTGTGC CCTCTGCCTG GACAAGCACA TAGCAAGCTG AACTGTCTTA 2040
AGGCAGGGGC GAGCACGGAA CAATGGGGCC TTCAGCTGGA GCTGTGGACT TTTGTACATA 2100
CACTAAAATT CTGAAGTTAA AAAAAAAAAA AAAAGGAATT C 2141

FIG.10

